SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: French, Cynthia K.
                  Schneider, Patrick A.
                  Yamamoto, Karen K.

    (ii) TITLE OF INVENTION: Prostate Cancer-Specific Marker

  (iii) NUMBER OF SEQUENCES: 2

   (iv) CORRESPONDENCE ADDRESS:
       (A) ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
       (B) STREET: Two Embarcadero Center, 8th Floor
       (C) CITY: San Francisco
       (D) STATE: CA
       (E) COUNTRY: USA
       (F) ZIP: 94111

    (v) COMPUTER READABLE FORM:
       (A) MEDIUM TYPE: Floppy disk
       (B) COMPUTER: IBM PC compatible
       (C) OPERATING SYSTEM: PC-DOS/MS-DOS
       (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
       (A) APPLICATION NUMBER: (to be assigned)
       (B) FILING DATE: (herewith)
       (C) CLASSIFICATION:

  (viii) ATTORNEY/AGENT INFORMATION:
       (A) NAME: Dow, Karen B.
       (B) REGISTRATION NUMBER: 29,684
       (C) REFERENCE/DOCKET NUMBER: 018002-000210US

   (ix) TELECOMMUNICATION INFORMATION:
       (A) TELEPHONE: 415-576-0200
       (B) TELEFAX: 415-576-0300

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3891 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 151..1425

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CTCTTTGCCT CCTCCCTGTT CCAGGAGCTG GTGCCCTGGG CTCTGCGCTG TTGTTTTCAG          60

CGTTCCGAAA GCCGGCGCTT GAGATCCAGG CAAGTGAATC CAGCCAGGCA GTTTTCCCTT         120

CAGCACCTCG GACAGAACAC GCAGTAAAAA ATG GCT CCG ATC ACC ACC AGC CGG         174
                                  Met Ala Pro Ile Thr Thr Ser Arg
                                   1               5

GAA GAA TTT GAT GAA ATC CCC ACA GTG GTG GGG ATC TTC AGT GCA TTT         222
Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe
         10              15                  20

GGC CTG GTC TTC ACA GTC TCT CTC TTT GCA TGG ATC TGC TGT CAG AGA         270
Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln Arg
 25              30                  35                  40

AAA TCA TCC AAG TCT AAC AAG ACT CCT CCA TAC AAG TTT GTG CAT GTG         318
Lys Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val
             45                  50                  55

CTT AAG GGA GTT GAT ATT TAC CCT GAA AAC CTA AAT AGC AAA AAG AAG         366
Leu Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys
                 60                  65                  70

TTT GGA GCA GAT GAT AAA AAT GAA GTA AAG AAT AAG CCA GCT GTG CCA         414
Phe Gly Ala Asp Asp Lys Asn Glu Val Lys Asn Lys Pro Ala Val Pro
             75                  80                  85

AAG AAT TCA TTG CAT CTG GAT CTT GAA AAG AGA GAT CTC AAT GGC AAT         462
Lys Asn Ser Leu His Leu Asp Leu Glu Lys Arg Asp Leu Asn Gly Asn
             90                  95                 100

TTT CCC AAA ACC AAC CTC AAA CCT GGC AGT CCT TCT GAT CTG GAG AAT         510
Phe Pro Lys Thr Asn Leu Lys Pro Gly Ser Pro Ser Asp Leu Glu Asn
105                 110                 115                 120

GCA ACC CCG AAG CTC TTT TTA GAA GGG GAA AAA GAG TCA GTT TCC CCT         558
Ala Thr Pro Lys Leu Phe Leu Glu Gly Glu Lys Glu Ser Val Ser Pro
                125                 130                 135

GAG AGT TTA AAG TCC AGC ACT TCC CTT ACT TCA GAA GAG AAA CAA GAG         606
Glu Ser Leu Lys Ser Ser Thr Ser Leu Thr Ser Glu Glu Lys Gln Glu
                140                 145                 150

AAG CTG GGA ACT CTC TTC TTC TCC TTA GAA TAC AAC TTC GAG AGA AAA         654
Lys Leu Gly Thr Leu Phe Phe Ser Leu Glu Tyr Asn Phe Glu Arg Lys
            155                 160                 165

GCA TTT GTG GTC AAT ATC AAG GAA GCC CGT GGC TTG CCA GCC ATG GAT         702
Ala Phe Val Val Asn Ile Lys Glu Ala Arg Gly Leu Pro Ala Met Asp
        170                 175                 180
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    GAG CAG TCG ATG ACC TCT GAC CCA TAT ATC AAA ATG ACG ATC CTC CCA      750
    Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr Ile Leu Pro
    185                 190             195                 200

5   GAG AAG AAG CAT AAA GTG AAA ACT AGA GTG CTG AGA AAA ACC TTG GAT      798
    Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr Leu Asp
                    205             210                 215

10  CCA GCT TTT GAT GAG ACC TTT ACA TTC TAT GGG ATA CCC TAC ACC CAA      846
    Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr Thr Gln
                220             225                 230

15  ATC CAA GAA TTG GCC TTG CAC TTC ACA ATT TTG AGT TTT GAC AGG TTT      894
    Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp Arg Phe
            235             240                 245

20  TCA AGA GAT GAT ATC ATT GGG GAA GTT CTA ATT CCT CTC TCG GGA ATT      942
    Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu Ser Gly Ile
        250             255             260

    GAA TTA TCT GAA GGA AAA ATG TTA ATG AAT AGA GAG ATC ATC AAG AGA      990
    Glu Leu Ser Glu Gly Lys Met Leu Met Asn Arg Glu Ile Ile Lys Arg
    265             270             275                 280

25  AAT GTT AGG AAG TCT TCA GGA CGG GGT GAG TTA CTG ATC TCT CTC TGC     1038
    Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu Leu Ile Ser Leu Cys
                    285             290                 295

30  TAT CAG TCC ACC ACA AAC ACT CTA ACT GTG GTT GTC TTA AAA GCT CGA     1086
    Tyr Gln Ser Thr Thr Asn Thr Leu Thr Val Val Val Leu Lys Ala Arg
                300             305                 310

35  CAT CTG CCT AAA TCT GAT GTG TCC GGA CTT TCA GAT CCC TAT GTC AAA     1134
    His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser Asp Pro Tyr Val Lys
            315             320                 325

    GTG AAC CTG TAC CAT GCC AAA AAG AGA ATC TCC AAG AAG AAG ACT CAT     1182
    Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser Lys Lys Lys Thr His
        330             335             340

40  GTG AAG AAA TGC ACC CCC AAT GCA GTG TTC AAT GAG CTG TTT GTC TTT     1230
    Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn Glu Leu Phe Val Phe
    345             350             355                 360

45  GAT ATT CCT TGT GAG GGC CTT GAA GAT ATA AGT GTT GAA TTT TTG GTT     1278
    Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser Val Glu Phe Leu Val
                365             370                 375

50  TTG GAT TCT GAA AGG GGG TCC CGA AAT GAG GTA ATC GGG CAG TTA GTC     1326
    Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu Val
                380             385                 390

55  TTG GGT GCA GCA GCA GAA GGA ACT GGT GGA GAG CAC TGG AAA GAG ATC     1374
    Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu Ile
            395             400                 405

    TGT GAC TAC CCC AGG AGA CAA ATT GCC AAG TGG CAC GTG CTC TGT GAT     1422
    Cys Asp Tyr Pro Arg Arg Gln Ile Ala Lys Trp His Val Leu Cys Asp
    410                 415                 420

60  GGT TAGCATCCTA GCCGTGAGTT GGAACTTAAA GGTTTTTACT AGGCAAGGAG          1475
    Gly
    425

65  AAATTTCTT TCTTTCTATA TTGGATTGCA AGCTTGGGAA ATCAAGCTAC CTTTTTGTTG    1535

    TTGTTGTTGT TGCTAGAAAT GGATTGAATT AGTAGACCAG AAAGTAACTT CAAATGTGTA   1595
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TTATGATAAT TTCCCTATTT ATTAGAAGAG TTGGATAAAT TTTCATAAGA TATTCAATAT    1655

CTCCTTCAGA TTACCAGTGA TATAACTAGG AATAGTCAGA CATTTTATGA ATACTGTGCC    1715

AGAATCCCAA ATTATAAATG TGACAATCTC ATTGGAACAT GTCACAAAAA GTTAATGTGA    1775

TTAAGATTTA AAAACGAAAA GTATGCCTTG CCTTGTGAAA ATTTATCCAT TTATCTTCAG    1835

GTTGGGGGAA ATCAATTTTT CTTTAATCCA AAGATACTAA AAAAATGTCC TCCAGTTTGT    1895

ATTTATTAAT TCTGTCATGT GCAAATGGTT GTCCTGCATA TAAAAGTATC TGGTCATTTC    1955

AGTTTGGTTT GTAATTATTT GATGCAATTT TATCATAAGA GTAACTCAGA TTCATTTCAA    2015

AAGGACAGTG AACAAGCTGA GAAATTATTT TATCAAAGGG CTGAGTTGAG AACACTGTGG    2075

CTGAAATATA ATTTTTCTCC CCCCTAAGGT TACATGTGAG TCAAAATTTT GTAAAATATA    2135

ACCTCACATA AGAACCATGG CCTTGGATTA TTCACTGCCT GTCACAAGCC TCAGTGTGGC    2195

CTGAGAAATC CCTATGTACC TTTGTGAAAT TGTTGAATTA GTTAGTGAAT AAAGAAATAA    2255

ACTTCAACTA GAAATCCAGT TAGAAGTGCA ATTTTCTTAT AGGAAATAGG TATAGTGTGC    2315

AAGTGTACTT TTAAGGCCAT CGTTTGTACC CAGAGTCGGC ATGGCCACCT AAGTCTTCAT    2375

TTAATTTATT GTCCCCCAGA AAAGATTAAG ATGCTACTTG AAAAGACTGT GAAGATTTTT    2435

TACATTGCCA GATAAAAAGT GTTACTTAAC CAACAAACAA ATGTAAGACT ACAAAATCGT    2495

TCAAGAGCAA TTCTAATATA ATTTACATAT GTTCACGCAA AATATGCTTA GGCTGTCAAA    2555

TTAGCACAAC AAAGAATGTG TTTCACTATC TTTTCTAGGC TAATTTGTCT TGAGCTGTTG    2615

TCTATAGAGC AGTTTACAGA CTTGTGTCTT GTATCATTTT CCAGTGCCAG GGTTCTGAAA    2675

TTCATTCAGA ACCTGTTAGA TTAAAGCTGC ACCCTGTGAT TATTTGAAAA GAATTAGCTT    2735

GAGAGTAATG TCACTATATT TGAGTTCTTA GAGAAGTATG AGTGGAACTT GAGTACAGTT    2795

GAATTATTAA ATATGCAAGT TAGAAATTAA GTCTACTGAA AAATTTACAT TTTGAGTCAG    2855

GTTTTGTGTC AGTACTTTAG CAGTTTTTGA GAATGTGTTT GATATCACAG TGTTTGTAAA    2915

TTCTATGAAA AATGCATTTT CCAAACAACT TATACATGCT TTTTATGACT ATGCCTAATG    2975

TAAAGAAAAT GTATTACATT CTGTATGTAC AAAGATTAAA AATCAACCTC TTTTTTGTGC    3035

TTTAAAATGA CTTTGGGATT AAAAAAGCAT ATTTCCCAAT CATTGTCTTC ATTCCACTAC    3095

AAAGTCACCT CACAGCATCT TGCTCCACTC GGCATCTCTG TGAAAGCAAC ATGAAATGAA    3155

CTGTAGTAGG TGTGTAGTTT GGGGAAGTCA AATGGCCATT TTATGTATGT GCATTTGGTA    3215

TCATGGGCCG TGGAACAGAA TATATGTTGG ACCTCTGAAA AGTTGTAAGG GGCCAAATCT    3275

AAGTATTCTT CACGGCAGCC AGAAGTTAAT GGTGGTAGCA GCTGAGGTAT GGTTGTTGGA    3335

CGAGGCCGAT TTTTTTTTTT TAACATGGAA CAATGAAACC AACAACAAAC ATTTTTAAAA    3395

TTAAAATGGA TAATTTGTAA ATAGTTTTTA GCTTTTAAAA TTTAAAGTGT TTTTGAGTGT    3455

GAAAAGTTGA GTAAACTAT TTGCAACTGG TTTTCAGAAA AGAGAAAAGA AACAACAAAG    3515

GAATTGAAAC AGGCAGGGAG ATCTTAATAC CTAATTTCAT CATTTCTGCA AAATGTACTG    3575

TTTTAGAATG TATTACAATA TCAATGTGAA TATCTTGAAT CCTGTTACAA ATCCTGCACT    3635
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GTATTAAACA TGTAAATTAA TTGTTTGTCT GATTAGCCAA TCTCACCACC CAAATGGGGA    3695

GGTATACATG TTTGAAGAAC GTGTAACTCG GTAATTGATT TGTTCTGATG TTGTAACTCA    3755

ATAGAAGTGT TTTGGAAGGA AGCATGGTGT GTGAGACAGT GTCTGTTCTT TTGTGCCAGC    3815

TCTGTATGAT GTTTGTAAGA CCATGTTTGT AAGACATGAA TAAATTGCTG CTTTTGCCCA    3875

AAAAAAAAAA AAAAA                                                     3891
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(2) INFORMATION FOR SEQ ID NO:2:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 425 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Ala Pro Ile Thr Thr Ser Arg Glu Glu Phe Asp Glu Ile Pro Thr
  1           5               10                  15

Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu
               20              25              30

Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr
           35              40              45

Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
       50              55              60

Glu Asn Leu Asn Ser Lys Lys Phe Gly Ala Asp Asp Lys Asn Glu
 65              70              75              80

Val Lys Asn Lys Pro Ala Val Pro Lys Asn Ser Leu His Leu Asp Leu
               85              90              95

Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Leu Lys Pro
              100             105             110

Gly Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu
              115             120             125

Gly Glu Lys Glu Ser Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser
       130             135             140

Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Phe Ser
145             150             155             160

Leu Glu Tyr Asn Phe Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu
              165             170             175

Ala Arg Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
          180             185             190

Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
       195             200             205

Arg Val Leu Arg Lys Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr
   210             215             220

Phe Tyr Gly Ile Pro Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe
225             230             235             240

Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu
              245             250             255

Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu
          260             265             270

Met Asn Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg
       275             280             285

Gly Glu Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu
       290             295             300
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    Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser
    305             310             315             320

5   Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys
                    325             330             335

    Arg Ile Ser Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala
                    340             345             350

10  Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu
                    355             360             365

    Asp Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg
                370             375             380

15  Asn Glu Val Ile Gly Gln Leu Val Leu Gly Ala Ala Ala Glu Gly Thr
    385             390             395             400

20  Gly Gly Glu His Trp Lys Glu Ile Cys Asp Tyr Pro Arg Arg Gln Ile
                    405             410             415

    Ala Lys Trp His Val Leu Cys Asp Gly
                    420             425
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